50. (New) A pharmaceutical composition comprising the isolated DNA of any one of claims 37, 38, 39, 48 or 49.

51. (New) A recombinant expression vector comprising the isolated nucleic acid of any one of claims 37, 38, 39, 48 or 49.

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52. (New) A host cell transformed with the recombinant vector of claim 51.

53. (New) A method of producing an NGSP polypeptide or fragment thereof, comprising culturing a host cell transformed with the recombinant vector of claim 51 and harvesting expressed NGSP polypeptide or fragment thereof.--

REMARKS

Upon entry of the present amendments, claims 37-39 and 48-53 will be pending and under active consideration. Claims 1-36 and 42-47 are cancelled without prejudice as directed to non-elected subject matter in accord with a requirement for restriction. New claims 48, 49 and 51-53 are added directed to certain embodiments of the elected invention. Claims 40 is cancelled without prejudice as it is redundant with claim 39 as amended. Claim 41 is cancelled without prejudice and replaced by new claim 50 to avoid dependency upon claims with a higher number. New claims 51-53 directed to recombinant expression vectors, host cells and a method for using the recombinant expression vectors containing the nucleic acid of claims 37, 38, 39, 48 or 49 are fully supported by the specification as filed, *e.g.*, in Section 5.7 at pages 31-33. Applicants reserve all rights to prosecute the subject matter of canceled claims in a subsequent continuation or divisional application.

Amendments to Specification and Claims

The text of the specification has been amended merely to avoid certain informalities regarding the Table of Contents, hyperlinks and trademarks. The text has also been amended to be consistent with the originally filed Sequence Listing, hence avoiding inconsistencies objected to in the Office Action. No new matter is added. In light of the amendments, it is submitted that the objections to the specification are avoided and should be withdrawn.

The claims have been amended not for any reason related to patentability. Rather, the claims have been amended to avoid dependence upon cancelled claims and to be consistent with the language of the specification. The amended claims and new claims 48-53 are fully supported by the specification and claims as originally filed and no new matter is added.

Objections to Claims

Claim 37 is objected to as dependent upon a non-elected claim and as lacking an article before the term "fragment" and claims 37-41 are objected to as including the subject matter of non-elected inventions.

As amended above herein, claims 37-39 and 50, which replaces claim 41, avoid all the reasons for the formal objections (not related to patentability) and it is respectfully requested that the formal objections be withdrawn.

Rejections

Claims 37, 38 and 41 are rejected under 35 USC 102(b) as allegedly anticipated by Lehninger (Principles of Biochemistry, Worth Publishers, Inc., New York,

Chapter 27, pp 793-836, 1982 "Lehninger"). It is alleged that claims 37, 38 and 41 encompass a fragment of DNA which is one nucleotide or base in length.

Attorneys for Applicants emphatically disagree and submit that this rejection is in error. This rejection must fail since the smallest encoded fragment described in the specification has at least 5 amino acids in length. Hence, the smallest nucleic acid fragment originally claimed has at least 15 nucleotides. Further, the claims have been amended to more particularly recite the subject matter described in the specification. Original claims 37, 38 and 41 did not claim a fragment of DNA encompassing anything less than at least 15 nucleotides and claims 37, 38, as amended and new claim 49 (and new claims 50-53 to the extent dependent on these claims) do not claim a fragment, but rather a molecule having a sequence which is SEQ ID NO:3. The DNA molecule claimed in claim 39 (and new claims 50-53 to the extent dependent thereon) must be complementary to at least 25 contiguous nucleotides of SEQ ID NO:3. The nucleic acid molecule claimed in newly added independent claim 48 (and new claims 50-53 to the extent dependent thereon) is not anticipated by Lehninger because the fragment encoded by said nucleic acid must comprise at least 7 amino acids of the polypeptide encoded SEQ ID NO:3.

For all of the above reasons, the single nucleotide taught by Lehninger cannot and does not anticipate the claimed nucleic acids. The reference does not teach or enable the subject matter of the claims as originally filed or as presently amended .

Claims 37, 38 and 41 are rejected under 35 USC 102(b) as allegedly anticipated by Cleton-Jansen et al., Mol. Gen. Genet. 229:206-212, 1991 "Cleton-Jansen". It is alleged that Cleton-Jansen teach a DNA fragment that shows 100% match with a fragment of SEQ ID NO:3 .

Attorneys for Applicants disagree. From reading the sequence search report, it would appear that the sequence taught by Cleton-Jansen encodes a protein which is a substrate of quinoprotein glucose dehydrogenase from *Gluconobacter oxydans*. The sequence taught by Cleton-Jansen is 2890 nucleotides in length. The search report shows that residues 340-359 of the sequence taught by Cleton-Jansen are 100% homologous to residues 597-616 of the SEQ ID NO:3 of the present application. The sequence taught by Cleton-Jansen does not encode an NGSP polypeptide as described in the specification. In fact, the sequence disclosed in Cleton-Jansen does not encode any polypeptide of *Neisseria* sp. Hence, the reference does not suggest, much less teach the subject matter of present claims 37, 38 and 49 (and new claims 50-53 to the extent dependent on these claims). Furthermore, claim 39 (and new claims 50-53 to the extent dependent thereon), as presently claimed, recites a nucleic acid which is complementary to at least 25 contiguous nucleotides of SEQ ID NO:3. With respect to newly added claim 48 (and new claims 50-53 to the extent dependent thereon), the claimed nucleic acid molecule encodes a polypeptide which is at least 7 amino acids in length. The portion of the nucleic acid of Cleton-Jansen cited by the Examiner is only 20 nucleic acids in length which can encode at most 6 amino acids. Therefore, the nucleic acid molecule claimed in claim 48 (and new claims 50-53 to the extent dependent thereon) is not anticipated by Cleton-Jensen. For all of the above reasons, the cited Cleton-Jansen sequence cannot and does not anticipate the present claims.

Claims 37, 38 and 41 are rejected under 25 USC 102(b) as allegedly anticipated by Matsubara et al. (WO 9514772) "Matsubara". It is alleged that Matsubara teach a fragment of a nucleotide sequence that shows 100% match with a fragment of the presently claimed isolated DNA having SEQ ID NO. 3.

Attorneys for Applicants disagree. From reading the sequence search report, it appears that Matsubara teach a DNA sequence which is 196 base pairs in length which is derived from a human cDNA library. The search report shows that residues 64-84 of the sequence taught by Matsubara are 100% homologous to residues 709-725 of the SEQ ID NO:3 of the present application. The sequence taught by Matsubara does not encode an NGSP polypeptide as described in the specification. In fact, it does not describe a nucleic acid that encodes any polypeptide of *Neisseria* sp. Furthermore, claims 37 and 38 (and new claims 50-53 to the extent dependent on these claims), as presently claimed, recite a nucleic acid having SEQ ID NO. 3. Claim 39 recites a nucleic acid which is complementary to at least 25 contiguous nucleotides of SEQ ID NO: 3. Such molecules are not disclosed by the cited fragment of Matsubara which is only 17 base pairs in length. With respect to newly added claim 48 (and new claims 50-53 to the extent dependent thereon), the claimed nucleic acid molecule encodes a polypeptide which is at least 7 amino acids in length. The portion of the nucleic acid of Matsubara cited by the Examiner is only 17 nucleic acids in length which can encode at most 5 amino acids. Therefore, the nucleic acid molecule claimed in claim 48 (and new claims 50-53 to the extent dependent thereon) is not anticipated by Matsubara. So far as Applicants can determine there is no teaching in Matsubara which suggests a fragment of the nucleic acid corresponding to the fragment which has homology to SEQ ID NO:3. Thus one with skill in the art would not have been motivated to make the cited 17 nucleic acid fragment of the DNA taught by Matsubara et al., much less, the presently claimed molecules, all having encoding at least 7 amino acids. For all of the above reasons, the cited Matsubara sequence cannot and does not anticipate the claimed nucleic acid.

Claims 38-41 are rejected under 35 USC 102(a) as allegedly anticipated by Billing-Medel (WO9818945, "Billing-Medel"). It is alleged that Billing-Medel disclose a

complement of a nucleotide sequence that shows 100% match with a fragment of the claimed isolated DNA having SEQ ID NO:3 and would be expected to hybridize to the sequence of SEQ ID NO:3.

Attorneys for Applicants do not agree. From the sequence search report, Billing-Medel disclose a 229 base pair nucleic acid encoding a protein which is a breast tissue antigen. The search report shows that residues 187-171 of the sequence taught by Billing-Medel are 100% homologous to residues 381-397 of the SEQ ID NO:3 of the present application. The sequence taught by Billing-Medel does not encode an NGSP polypeptide, nor even a sequence encoding any polypeptide of *Neisseria* sp. Furthermore the claims, as presently claimed, recite a nucleic acid which is complementary to at least 25 contiguous nucleotides of SEQ ID NO: 3. Such a molecule is not disclosed by the cited fragment of Billing-Medel which is only 17 base pairs in length. With respect to newly added claim 48 (and new claims 50-53 to the extent dependent thereon), the claimed nucleic acid molecule encodes a polypeptide which is at least 7 amino acids in length. Therefore, the nucleic acid molecule claimed in claim 48 (and new claims 50-53 to the extent dependent thereon) is not anticipated by Billing-Medel. The portion of the nucleic acid of Billing-Medel cited by the Examiner is only 17 nucleic acids in length which can encode at most 5 amino acids. So far as Applicants can determine there is no teaching in Billing-Medel which suggests that a fragment of the nucleic acid corresponding to the fragment which has homology to SEQ ID NO:3 should be constructed. For all of the above reasons, the cited Billing-Medel sequence cannot and does not anticipate the claimed nucleic acid.

In view of the above, it is submitted that all the rejections based on Section 102 are in error and have been avoided.

Further, it is submitted that the claims are in form for allowance and action to that end is requested.

Respectfully submitted,

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